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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/930,329

DATE: 08/27/2001
TIME: 12:24:40

Input Set : D:\008010103DVUS02.txt
Output Set: N:\CRF3\08272001\I930329.raw

4 <110> APPLICANT: TURPEN, Thomas H.
6 <120> TITLE OF INVENTION: VIRAL AMPLIFICATION OF RECOMBINANT
7 MESSENGER RNA IN TRANSGENIC PLANTS
10 <130> FILE REFERENCE: 008010103DVUS02
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/930,329
13 <141> CURRENT FILING DATE: 2001-08-14
15 <150> PRIOR APPLICATION NUMBER: 09/414,916
16 <151> PRIOR FILING DATE: 1999-10-08
18 <150> PRIOR APPLICATION NUMBER: 08/336,724
19 <151> PRIOR FILING DATE: 1994-11-09
21 <160> NUMBER OF SEQ ID NOS: 3
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1824
27 <212> TYPE: RNA
28 <213> ORGANISM: Tobacco Mosaic Virus
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (70)...(873)
33 <223> OTHER INFORMATION: (episomal) peptide encodes fo TMV 30kDa movement
34 protein (268 residues) and CAT (204 residues).
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (916)...(1530)
39 <400> SEQUENCE: 1
40 guauuuuuuac aacaauuacc aacaacaaca aacaacaaac aacauuacaa uuacuauuuu 60
41 caauuacau aug gcu cua guu guu aaa gga aaa gug aa uuc aa u gag uuu 111
42 Met Ala Leu Val Val Lys Gly Lys Val Asn Ile Asn Glu Phe
43 1 5 10
45 auc gac cug aca aaa aug gag aag auc uua ccg ucg aug uuu acc ccu 159
46 Ile Asp Leu Thr Lys Met Glu Lys Ile Leu Pro Ser Met Phe Thr Pro
47 15 20 25 30
49 gua aag agu guu aug ugu ucc aaa guu gau aaa aua aug guu cau gag 207
50 Val Lys Ser Val Met Cys Ser Lys Val Asp Lys Ile Met Val His Glu
51 35 40 45
53 aau gag uca uug uca gag gug aac cuu uuu aaa gga guu aag cuu auu 255
54 Asn Glu Ser Leu Ser Glu Val Asn Leu Phe Lys Gly Val Lys Leu Ile
55 50 55 60
57 gau agu gga uac guc ugu uua gcc ggu uug guc guc acg ggc gag ugg 303
58 Asp Ser Gly Tyr Val Cys Leu Ala Gly Leu Val Val Thr Gly Glu Trp
59 65 70 75
61 aac uug ccu gac aa ugc aga gga ggu gug agc gug ugu cug gug gac 351
62 Asn Leu Pro Asp Asn Cys Arg Gly Gly Val Ser Val Cys Leu Val Asp
63 80 85 90
65 aaa agg aug gaa aga gcc gac gag gcc acu cuc ucu uac uac aca 399
66 Lys Arg Met Glu Arg Ala Asp Glu Ala Thr Leu Gly Ser Tyr Tyr Thr
67 95 100 105 110
69 gca gcu gca aag aaa aga uuu cag uuc aag guc guu ccc aa u au gcu 447

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70	Ala	Ala	Ala	Lys	Lys	Arg	Phe	Gln	Phe	Lys	Val	Val	Pro	Asn	Tyr	Ala	
71					115					120					125		
73	aua	acc	acc	cag	gac	gcg	aug	aaa	aac	guc	ugg	caa	guu	uua	guu	aaU	495
74	Ile	Thr	Thr	Gln	Asp	Ala	Met	Lys	Asn	Val	Trp	Gln	Val	Leu	Val	Asn	
75				130					135					140			
77	auu	aga	aaU	gug	aag	aug	uca	gcg	ggU	uuc	ugu	ccg	cuu	ucu	cug	gag	543
78	Ile	Arg	Asn	Val	Lys	Met	Ser	Ala	Gly	Phe	Cys	Pro	Leu	Ser	Leu	Glu	
79				145				150					155				
81	uuu	gug	ucg	gug	ugu	auu	guu	uau	aga	aaU	aaU	aua	aaa	uua	ggU	uug	591
82	Phe	Val	Ser	Val	Cys	Ile	Val	Tyr	Arg	Asn	Asn	Ile	Lys	Leu	Gly	Leu	
83		160					165					170					
85	aga	gag	aag	auu	aca	aac	gug	aga	gac	gga	ggg	ccc	aug	gaa	cuu	aca	639
86	Arg	Glu	Lys	Ile	Thr	Asn	Val	Arg	Asp	Gly	Gly	Pro	Met	Glu	Leu	Thr	
87	175					180				185					190		
89	gaa	gaa	guc	guu	gau	gag	uuc	aug	gaa	gau	guc	ccu	aug	ucg	auc	agg	687
90	Glu	Glu	Val	Val	Asp	Glu	Phe	Met	Glu	Asp	Val	Pro	Met	Ser	Ile	Arg	
91				195					200				205				
93	cuu	gca	aag	uuu	cga	ucu	cga	acc	gga	aaa	aag	agu	gau	guc	cgc	aaa	735
94	Leu	Ala	Lys	Phe	Arg	Ser	Arg	Thr	Gly	Lys	Lys	Ser	Asp	Val	Arg	Lys	
95			210					215					220				
97	ggg	aaa	aaU	agu	agu	aaU	gau	cgg	uca	gug	ccg	aac	aag	aac	uau	aga	783
98	Gly	Lys	Asn	Ser	Ser	Asn	Asp	Arg	Ser	Val	Pro	Asn	Lys	Asn	Tyr	Arg	
99			225				230					235					
101	aaU	guu	aag	gau	uuu	gga	gga	aug	agu	uuu	aaa	aag	aaU	aaU	uua	auc	831
102	Asn	Val	Lys	Asp	Phe	Gly	Gly	Met	Ser	Phe	Lys	Lys	Asn	Asn	Leu	Ile	
103		240				245					250						
105	gau	gau	gau	ucg	gag	gcu	acu	guc	gcc	gaa	ucg	gau	ucg	uuu			873
106	Asp	Asp	Asp	Ser	Glu	Ala	Thr	Val	Ala	Glu	Ser	Asp	Ser	Phe			
107	255				260				265								
109	uaaaUacgcU	cgacgagauu	uucaggagcu	aaggaagcu	aa	aug	gag	aaa	aaa								927
110							Met	Glu	Lys	Lys							
111							270										
113	auc	acu	gga	uau	acc	acc	guu	gau	aua	ucc	caa	ucg	cau	cgu	aaa	gaa	975
114	Ile	Thr	Gly	Tyr	Thr	Thr	Val	Asp	Ile	Ser	Gln	Ser	His	Arg	Lys	Glu	
115			275				280					285					
117	cau	uuu	gag	gca	uuu	cag	uca	guu	gcu	caa	ugu	acc	uau	aac	cag	acc	1023
118	His	Phe	Glu	Ala	Phe	Gln	Ser	Val	Ala	Gln	Cys	Thr	Tyr	Asn	Gln	Thr	
119			290			295					300						
121	guu	cag	cug	gau	auu	acg	gcc	uuu	uua	aag	acc	gua	aag	aaa	aaU	aag	1071
122	Val	Gln	Leu	Asp	Ile	Thr	Ala	Phe	Leu	Lys	Thr	Val	Lys	Lys	Asn	Lys	
123	305				310					315					320		
125	cac	aag	uuu	uau	ccg	gcc	uuu	auu	cac	auu	cuu	gcc	cgc	cug	aug	aaU	1119
126	His	Lys	Phe	Tyr	Pro	Ala	Phe	Ile	His	Ile	Leu	Ala	Arg	Leu	Met	Asn	
127				325				330				335					
129	gcu	cau	ccg	gaa	uuc	cgu	aug	gca	aug	aaa	guu	uuc	cau	gag	caa	acu	1167
130	Ala	His	Pro	Glu	Phe	Arg	Met	Ala	Met	Lys	Val	Phe	His	Glu	Gln	Thr	
131			340					345				350					
133	gaa	acg	uuu	uca	ucg	cuc	ugg	agu	gaa	uac	cac	gac	gau	uuc	cgg	cag	1215
134	Glu	Thr	Phe	Ser	Ser	Leu	Trp	Ser	Glu	Tyr	His	Asp	Asp	Phe	Arg	Gln	

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135          355          360          365
137 uuu cua cac aua uau ucg caa gau gug gcg ugu uac ggu gaa aac cug      1263
138 Phe Leu His Ile Tyr Ser Gln Asp Val Ala Cys Tyr Gly Glu Asn Leu
139          370          375          380
141 gcc uau uua ccu aaa ggg uuu auu gag aaU aug uuu uuc guc uca gcc      1311
142 Ala Tyr Leu Pro Lys Gly Phe Ile Glu Asn Met Phe Phe Val Ser Ala
143 385          390          395          400
145 aaU ccc ugg gug agu uuc acc agu uuu gau uua aac gug gcc aaU aug      1359
146 Asn Pro Trp Val Ser Phe Thr Ser Phe Asp Leu Asn Val Ala Asn Met
147          405          410          415
149 gac aac uuc uuc gcc ccc guu uuc acc aug ggc aaa uau uau acg caa      1407
150 Asp Asn Phe Phe Ala Pro Val Phe Thr Met Gly Lys Tyr Tyr Thr Gln
151          420          425          430
153 ggc gac aag gug cug aug ccg cug gcg auu cag guu cau cau gcc guc      1455
154 Gly Asp Lys Val Leu Met Pro Leu Ala Ile Gln Val His His Ala Val
155          435          440          445
157 ugu gau ggc uuc cau guc ggc aga aug cuu aaU gaa uua caa cag uac      1503
158 Cys Asp Gly Phe His Val Gly Arg Met Leu Asn Glu Leu Gln Gln Tyr
159          450          455          460
161 ugc gau gag ugg cag ggc ggg gcg uaa uuuuuuuuag gcaguuauug      1550
162 Cys Asp Glu Trp Gln Gly Ala *
163 465          470
165 gugccuuaaa cgccuggugc uacgccugaa uaagugauaa uaagcggaug aauggcagaa      1610
166 auucgucgag gguagucaag augcauaaau aaUaacggau uguguccgua aucacacgug      1670
167 gugcguacga uaacgcuaug uguuuuuuccc uccacuuaaa ucgaagggguu gugucuugga      1730
168 ucgcgcgggu caaauguaua ugguucauau acauccgcag gcacguaaua aagcgagggg      1790
169 uucgaauccc cccguuaccc ccgguagggg ccca      1824
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 268
173 <212> TYPE: PRT
174 <213> ORGANISM: Tobacco Mosaic Virus
176 <400> SEQUENCE: 2
177 Met Ala Leu Val Val Lys Gly Lys Val Asn Ile Asn Glu Phe Ile Asp
178 1          5          10          15
179 Leu Thr Lys Met Glu Lys Ile Leu Pro Ser Met Phe Thr Pro Val Lys
180          20          25          30
181 Ser Val Met Cys Ser Lys Val Asp Lys Ile Met Val His Glu Asn Glu
182          35          40          45
183 Ser Leu Ser Glu Val Asn Leu Phe Lys Gly Val Lys Leu Ile Asp Ser
184          50          55          60
185 Gly Tyr Val Cys Leu Ala Gly Leu Val Val Thr Gly Glu Trp Asn Leu
186 65          70          75          80
187 Pro Asp Asn Cys Arg Gly Gly Val Ser Val Cys Leu Val Asp Lys Arg
188          85          90          95
189 Met Glu Arg Ala Asp Glu Ala Thr Leu Gly Ser Tyr Tyr Thr Ala Ala
190          100          105          110
191 Ala Lys Lys Arg Phe Gln Phe Lys Val Val Pro Asn Tyr Ala Ile Thr
192          115          120          125
193 Thr Gln Asp Ala Met Lys Asn Val Trp Gln Val Leu Val Asn Ile Arg

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194      130      135      140
195 Asn Val Lys Met Ser Ala Gly Phe Cys Pro Leu Ser Leu Glu Phe Val
196 145      150      155      160
197 Ser Val Cys Ile Val Tyr Arg Asn Asn Ile Lys Leu Gly Leu Arg Glu
198      165      170      175
199 Lys Ile Thr Asn Val Arg Asp Gly Gly Pro Met Glu Leu Thr Glu Glu
200      180      185      190
201 Val Val Asp Glu Phe Met Glu Asp Val Pro Met Ser Ile Arg Leu Ala
202      195      200      205
203 Lys Phe Arg Ser Arg Thr Gly Lys Lys Ser Asp Val Arg Lys Gly Lys
204      210      215      220
205 Asn Ser Ser Asn Asp Arg Ser Val Pro Asn Lys Asn Tyr Arg Asn Val
206 225      230      235      240
207 Lys Asp Phe Gly Gly Met Ser Phe Lys Lys Asn Asn Leu Ile Asp Asp
208      245      250      255
209 Asp Ser Glu Ala Thr Val Ala Glu Ser Asp Ser Phe
210      260      265
212 <210> SEQ ID NO: 3
213 <211> LENGTH: 204
214 <212> TYPE: PRT
215 <213> ORGANISM: Tobacco Mosaic Virus
217 <400> SEQUENCE: 3
218 Met Glu Lys Lys Ile Thr Gly Tyr Thr Thr Val Asp Ile Ser Gln Ser
219 1      5      10      15
220 His Arg Lys Glu His Phe Glu Ala Phe Gln Ser Val Ala Gln Cys Thr
221      20      25      30
222 Tyr Asn Gln Thr Val Gln Leu Asp Ile Thr Ala Phe Leu Lys Thr Val
223      35      40      45
224 Lys Lys Asn Lys His Lys Phe Tyr Pro Ala Phe Ile His Ile Leu Ala
225      50      55      60
226 Arg Leu Met Asn Ala His Pro Glu Phe Arg Met Ala Met Lys Val Phe
227 65      70      75      80
228 His Glu Gln Thr Glu Thr Phe Ser Ser Leu Trp Ser Glu Tyr His Asp
229      85      90      95
230 Asp Phe Arg Gln Phe Leu His Ile Tyr Ser Gln Asp Val Ala Cys Tyr
231      100      105      110
232 Gly Glu Asn Leu Ala Tyr Leu Pro Lys Gly Phe Ile Glu Asn Met Phe
233      115      120      125
234 Phe Val Ser Ala Asn Pro Trp Val Ser Phe Thr Ser Phe Asp Leu Asn
235      130      135      140
236 Val Ala Asn Met Asp Asn Phe Phe Ala Pro Val Phe Thr Met Gly Lys
237 145      150      155      160
238 Tyr Tyr Thr Gln Gly Asp Lys Val Leu Met Pro Leu Ala Ile Gln Val
239      165      170      175
240 His His Ala Val Cys Asp Gly Phe His Val Gly Arg Met Leu Asn Glu
241      180      185      190
242 Leu Gln Gln Tyr Cys Asp Glu Trp Gln Gly Gly Ala
243      195      200

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/930,329

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TIME: 12:24:41

Input Set : D:\008010103DVUS02.txt

Output Set: N:\CRF3\08272001\I930329.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number